

100605
16086 U.S. PTO

Ian S. Zagon, et al.
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Replacement Sheet

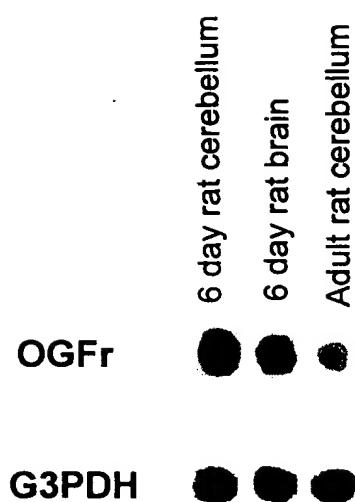


Figure 1

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 LeuSerArgArgGluLeuProProThrGlyProGlyProGlyProGly
 CCTCAGCCAGGCTCAGGACGGGACCCAGGAACACTGGGGCTCAGGACCCCTGGGAGCAGTCGCTGGCAACCCCTGGG 1350
 LeuSerGlyLeuArgThrGlyLeuAlaSerGlyLeuAlaSerAlaSerAla
 AGCAGGGGGCCGACAAGGTGAGGAGGGAGGAAGGCTGATGAGGGTACTGGGACACTGGCTGGCCAGTCGCTGGCCAGAC 1440
 AlaArgValAlaAspLeuValArgThrGlyLeuAlaAspProGlyGlyGlyLeuGly
 CTTGGCCCTGCGGGTCCCCTGCCATGGGCAAGGCTGGACACAGTGGAGACACAGTGGAGACACAGGAGCAAGGCTGG 1530
 LeuAlaLeuAlaGlyLeuProAlaLeuProSerGlyHisProLysAlaGlyHis
 GGGCCAAAGAAAGGTACCCCTGGAGGCCATGGGCAAGGCCAGGACACAGTGGAGACACAGGAGCAAGGCTGG 1620
 GlyProAlaGlyLeuProGlyLeuThrProGlyProGlyProAlaGlyProAlaGly
 GTCGGAGACCCCAGGCCAGGACCTACAAGGGATGAGCCAGGCCATGGAGACGCCAGGGCCAGGGCCAGGGGGGGGGGG 1710
 SerGlyLeuThrProGlyProGlyProAlaGlyAspGluProAlaLysLeuPro
 ATCGGAGACCCCAGGCCAGGACCTACAAGGGATGAGCCAGGCCATGGAGACGCCAGGGCCAGGGGGGGGGGGGGGGGG 1800
 ProAlaGlyAspGluLeuProSerProAlaGlyProGlyProAlaGly
 ATCGGAGACCCCAGGCCAGGACCTACAAGGGATGAGCCAGGCCATGGAGACGCCAGGGCCAGGGGGGGGGGGGGGGGG 1890
 SerGlyLeuThrProGlyProAlaGlyProThrArgAspGluProAlaGlyProAlaGly
 ACCTGCAGGGAGCGCCAGGCCATGGAGACGCCAGGGCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1980
 ProAlaGlyAspGluProAlaGlyLeuProAlaGlyProArgProAlaGlyAspGluProAlaGly
 ATCGGAGACCCCAGGCCAGGACCTACAAGGGATGAGCCAGGCCATGGAGACGCCAGGGCCAGGGGGGGGGGGGGGGGG 2070
 SerGlyLeuThrProGlyProAlaGlyProThrArgAspGluProAlaGlyLeuVal
 CGAGTCCTGCCCAGTCGGAAAGCCCTTAAGGAAAGGACTGCCGTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGG 2160
 GluSerAlaLysSerGlyLeuPro
 CGCTGGCCGCGG 2250
 CGCTGGCCGCGG 2340
 CGCCCTGCTTGTAAATTGACCTTGTAAATTGACCTTGTGGAGTGGGGGGGG 2382

B

Figure 8B

Figure 8B

A		1260
389	GCTGAGCCGGGGAGCAGGCCACAGGCCAGGCCCTCAGAGTCAGCTCAGGGAGAAGATCGCTGAAATTGGAGGGTGTGCC LeuSerArgArgGluInProProThrGlyProGlnSerAlaSerGluValGluLysIleAlaLeuAsnLeuGluGlyCysAla	
419	CCTCAGCCAGGGCAGCCCTCAGGACGGGACCCAGGAAGTGGCCAGGACCTGGGGAGGCACTGAGCCCTGGCCAAACCCCTGGG LeuSerGlnGlySerLeuArgThrGlyThrGlnGluValGlyGlyGlnAspProGlyGluAlaValGlnProGlyAsnGlnProLeuGly	
449	AGCCAGGGTGGCCGACAAGGTGAGGAGGGAGGGAGGTGGATGAGGGACAGTGGGGAGCTGGGTGGCCAGCTGGGGTGGCCAGAC AlaArgValAlaAspLysValArgLysValAspGluGlyThrGlyAspSerAlaAlaValAlaSerGlyGlyAlaGlnThr	
479	CTTGCCCTTGCGGGTCCCTGCCCCATCGGGCAACCCCAAGGGCAACAGTGAGAACAGGGTGGAGGAGAACAGGGTGGAGGAG LeuAlaLeuAlaGlySerProAlaProSerGlyHisProLysAlaGlyHisSerGluAsnGlyValGluGluAspThrGluGlyArgThr	
509	GGGCCAAAGAGGTAACCCCTGGGAGCCATGGAGAACCCCAAGGCCAGGCCAGGACGAGCCAGGCCAGGCAAGACCCCC GlyProLysGluGlyThrProGlySerProSerGluThrProAlaGlyProAlaGlyAspGluProAlaLysThrPro	
539	GTGGGAGACCCCCAGGGCCAGGGACCTACAGGGATGAGCCAGGCCAGGCCAGGCCATCGGGAGGCCAGGCCAGGCCAGGCC SerGluThrProGlyProSerProAlaGlyProSerProThrArgAspGluProAlaGluUserProAlaGluUserProAlaGlu	
569	GCAGGACCTCTGAGGGACGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC ProAlaGlyAspGluProAlaGluUserProSerGluThrProGlyProArgProAlaGlyProAlaGlyProSerGluThrProGly	
599	ATCGGAGACCCCCAGGGCCAGGACCTACAGGGATGAGCCAGGCCAGGCCAGGCCATCGGGAGGCCAGGCCAGGCCAGGCC SerGluThrProGlyProSerProAlaGlyProThrArgAspGluProAlaGluUserProSerGluThrProGlyProArgProAlaGly	
629	ACCTGAGGGCACGGCCAGGCCATGGAGACCCAGGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC ProAlaGlyAspGluProAlaGluUserProSerGluThrProGlyProArgProAlaGlyProAlaGlyProSerGluThrProGly	
659	CAGAGTTCGAGGGACGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC SerGluThrProGlyProSerProAlaGlyProAlaGlyProAlaGlyProAlaGluUserProAlaGluUserProAlaGlu	
689	GGAGTCCTGCTCAGGCAAGCTCTGGAAAGCCCTTAAGGAAAGGAGTGCCTGGCCGTCCTGGCTCTGGCTCTGGCTCTGGCTCTGGCT GluUserSerAlaLysSerGlyLysPro	
719	GGCCAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCC Gly	

Figure 8B

Figure 8B

Figure 8A

Figure 8A

A

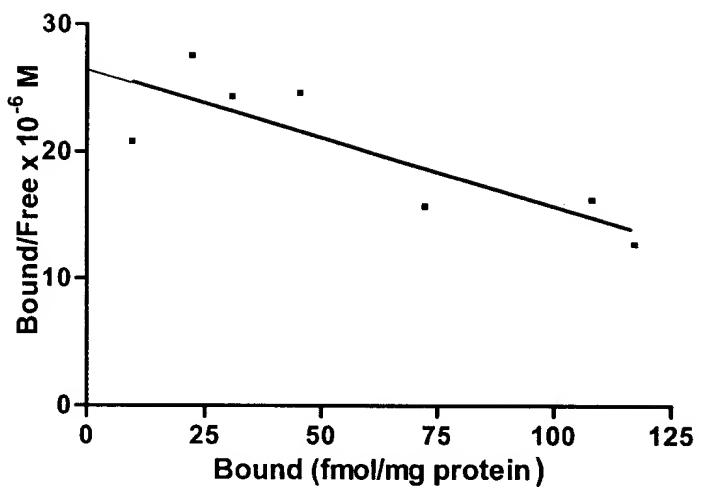


Figure 7B

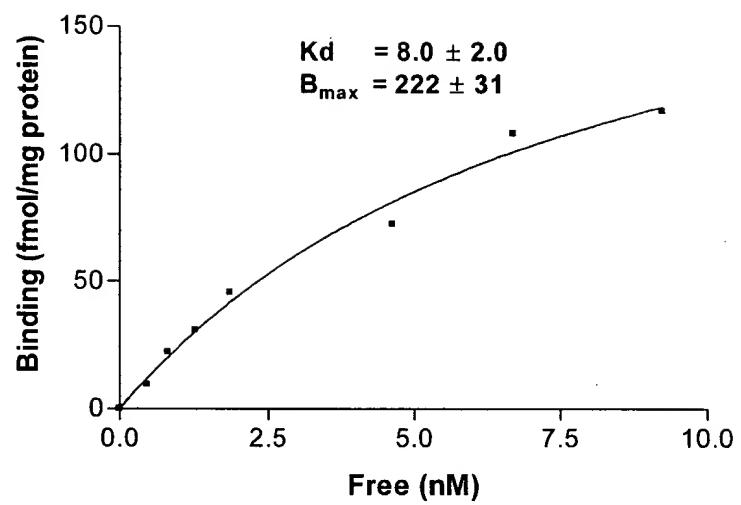


Figure 7A

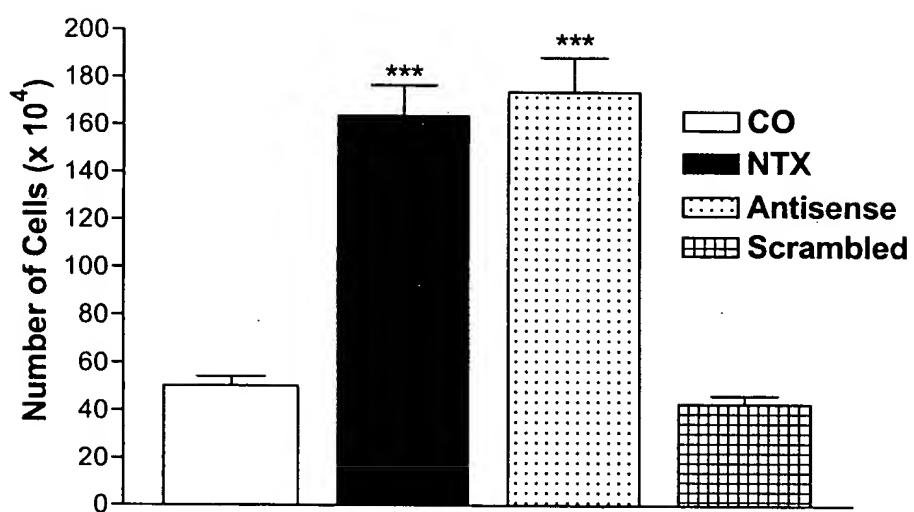


Figure 6

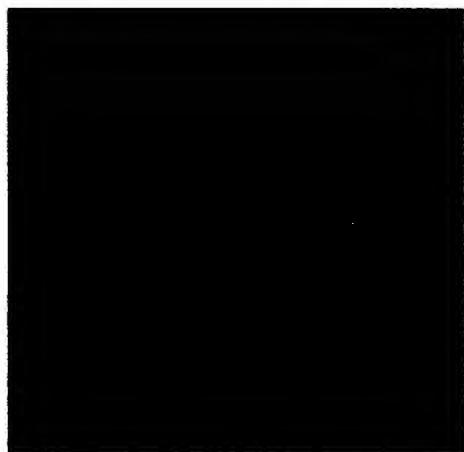
Figure 5A



Figure 5B



Figure 5C



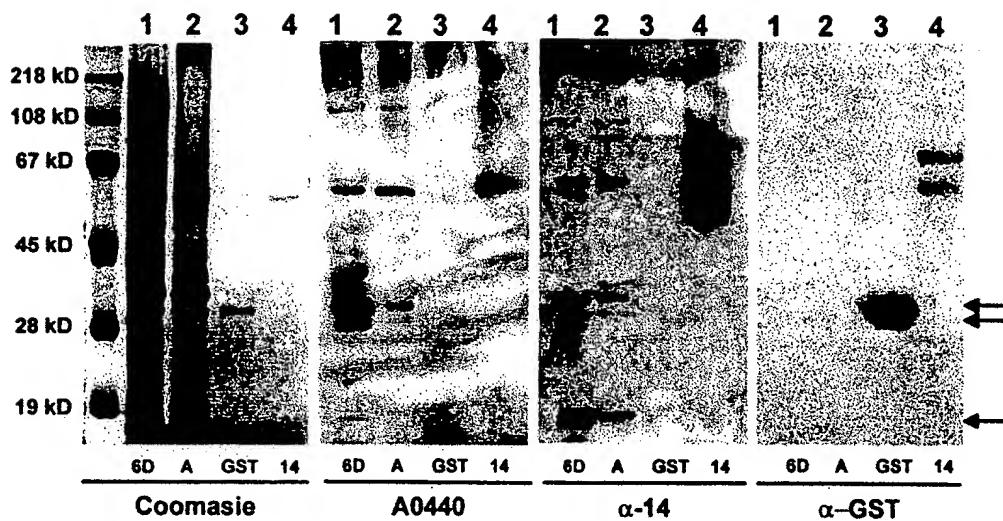


Figure 4A Figure 4B Figure 4C Figure 4D

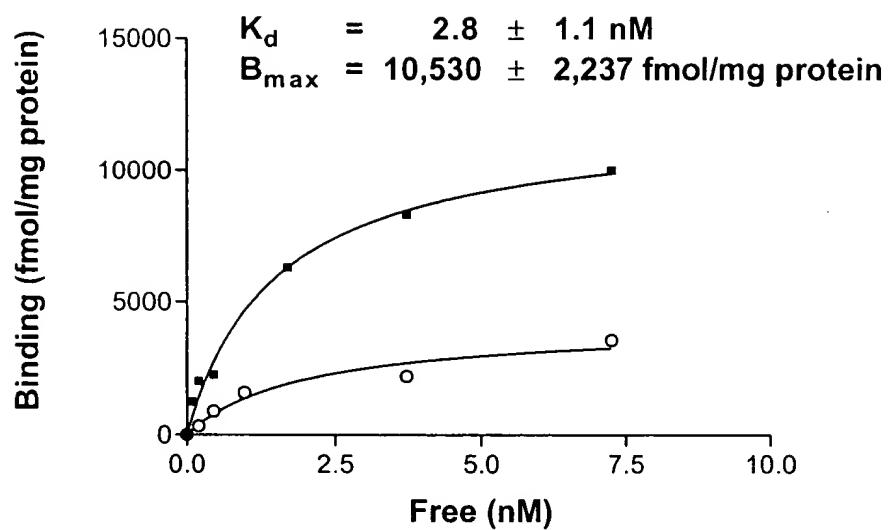


Figure 3

4

11111	-GAGGGAAACAGCCAGGACCACGTCACGGGAGGCATCCACGGGACATCCCCACGGTCTCTGAGCTAGAGAAAATGCCCTAACCTTGAGGACTGT GluglyAsnArgGlnGluGlnValProGlyGluAlaAsp <u>ProGlnGly</u> ValSerGluValGluLysileAlaLeuAsnLeuGluGluCys	400
11201	-GCCCTTAGCCCTATGCCAGGAGCCAGGGAGGTGACCCGCCATGGCTGCTGCTGAGCTAACACTCAATGAGCCAGTGCCTGCCTTACCCCTCAGACTGTCTGAG AlaLeuSerProIleSerGlnGluProArgGluAlaGluProProCys <u>ProValAlaAsnGluValArgLys</u> ArgArgLys	430
11291	-GTGGAGGAACGGGTGATGGAGTAGTCAGTAACACTCAATGAGCCAGTGCCTGCCTGCCTTACCCCTCAGACTGTCTGAGCTGTCTGAG ValGluGluGlyAlaGluGlyAsp <u>glyValValSerAsnThrGlnMetGlnAlaSerAlaLeuProProThrProSerGluCysProGlu</u> ProGlu AlaGlnLys <u>AspGlyAsnGly</u> ProGluAsp <u>AsnSerGlnValGly</u> ProGluAsp <u>AsnSerGlnValGly</u> ProGluAsp <u>ProAsnSerGlnVal</u>	460
11381	-GCCAAAAGGATGGAAATGGCCAGGACTCAAACGCCAGGTGGCCAGGCAATTCCAAAAGCCAGCTGGCCAGGGATCCAAACAGCCAGG AlaGlnLys <u>AspGlyAsnGly</u> ProGluAsp <u>AsnSerGlnValGly</u> ProGluAsp <u>AsnSerGlnValGly</u> ProGluAsp <u>AsnSerGlnVal</u>	490
11471	-AGCCAGCTGGGGCTGGAGGACCCAAACAGCCAGCTGGCCAGAGGACCCAAACAGCCAGGTGGCCAGAGGACCCAGAGGACCCAAACAGCCAGG SerGlnValGlyLeuGluAsp <u>ProAsnSerGlnValGly</u> ProGluAsp <u>ProAsnSerGlnValGly</u> ProGluAsp <u>ProAsnSerGlnVal</u>	520
11561	-GGCCAGAGGACCCAAACAGCCAGGTGGCCAGAGGACCCAAACAGCCAGGTGGCCAGAGGACCCAGGCAAGCTGCCCTCTAAGAGCCCTGTG Gly <u>ProGluAspProAsnSerGlnValGly</u> ProGluAsp <u>AsnSerGlnValGly</u> ProGluAsp <u>AsnSerGlnValGly</u> ProGluAsp <u>ProAsnSerGlnVal</u>	550
11651	-GAGGACCTGCACTATGCCAACCTCACTGGATGAGTCAGGAGTGGCAAGGATTGAGGCTCTGCTGAACCCCCAAAGCCT GluAsp <u>ProAspSerAspThrMetGlyThrSerValAspGluSerGluLeuAlaArgIleGluAlaSerAlaGluProProLysPro</u>	580
11741	-TAGAGGTGCACTCTCAGTCCACTGCCCCACTGCAAGGGGTTTCTGAGTCCAGGCTCTGCCGTTGCTGAGCTCTTCTGCTGAGCTCTGCCACAGTGC -TGCCTCTCCCTAGTGGTCACTGAGGTGGCACCCAGGGACTGAGGCCCCTGCCCTCAGGGCAAGGCCTTCAGAACCCCTCTAAC	610
11831	-CTRACTGTGTCCTCTCCTCACTGCCCTCTGAGCCCTGGTTGATCAGACCTTAAGGGCTTAGGGAGCCCCCTTCAATTAGTCTGGT -GCCAAAGTGAAGCCCTTTCTGAATAAACCTCTTGAACCTTGTCAAACCCCCAAAGCCTTAAGGGCTTAGGGAGCCCCCTTCAATTAGTCTGGT	640
11921	-GCCAAAGTGAAGCCCTTTCTGAATAAACCTCTTGAACCTTGTCAAACCCCCAAAGCCTTAAGGGCTTAGGGAGCCCCCTTCAATTAGTCTGGT -GCCAAAGTGAAGCCCTTTCTGAATAAACCTCTTGAACCTTGTCAAACCCCCAAAGCCTTAAGGGCTTAGGGAGCCCCCTTCAATTAGTCTGGT	670
20111	-GCCAAAGTGAAGCCCTTTCTGAATAAACCTCTTGAACCTTGTCAAACCCCCAAAGCCTTAAGGGCTTAGGGAGCCCCCTTCAATTAGTCTGGT -GCCAAAGTGAAGCCCTTTCTGAATAAACCTCTTGAACCTTGTCAAACCCCCAAAGCCTTAAGGGCTTAGGGAGCCCCCTTCAATTAGTCTGGT	700

88

Figure 2B

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-150 - TGGGCTCAGCCACGCCCAAGGTGCCCCAGCTGGGACTAGTTCTCATTCTGGCAGCTGCACACATCTGTCACTGAGGGAAATGTCAGGGT
-60 - TCTCACTCTCCTCTCACTATCCTTCCGAGAAAGGGGGATCTGCTGAGTATGGACGACCCGGACTGGGATTCCACCTGG
MetAspAspProAspCysAspSerThrTrp 10

31 - GAGGAGGAGCGAGGAGGATGGCCAGGATGACGGCGATGACGGCGATGAGGACACGGGGACGATGACGGGACGGGAGGAG
GluGluGluSerGluGluAspGlyGluAspGlyGlnAlaAspAspThrThrAspGluAspThrGlyAspAsp 40

121 - CCACGGCCAAGCCTGTTCCAGTCAGGATGACAGGGTACCGGAAACTGGCGTATGGCTATGGGACATGGGACAAACTACCCG
AlaArgProSerLeuPheGlnSerArgMetThrGlyTyrArgAsnTrpArgAlaMetGlnAspMetGlnArgTyrArgHisAsnTyrPro 70

211 - GATTGACAGATCAAGACTGCAATGGTGACATGGCTGAACTGAGCTTACAAAATGAGATCTGCTTCCAGCCAATGGGGCTCTCATC
AspLeuThrAspGlnAspCysAsnGlyAspMetCysAsnLeuSerPheTyrLysAsnGluIleCysPheGlnProAsnGlyAlaLeuIle 100

301 - GAGGACATTCTTCAGAAAGACAACTATGACCTCCTGAAAGAGAAATCACTCCTACATCCAGTGGCTGTTCTGCGGGAAACCA
GluAspIleLeuGlnAsnTrpLysAspAsnTyrAspLeuLeuGluAsnHisSerTyrIleGlnTrpLeuPheProLeuArgGluPro 130

391 - GCACTGGCACGCCAAGCCCTCACCCCTGAGGAGGTGAGGCCATTAAAGCTCCAAGGAAGTCAGAGGGCTCTGTCCGGGCC
GlyValAsnTrpHisAlaLysProLeuThrLeuLysGluValGluAlaPheLysSerSerLysGluValArgGluArgLeuValArgAla 160

481 - TATGAGCTCATGCTGGGCTCTATGGGTTCACCTTGAGGACCGGGCACGGGTGCTGTATGCCGTGACAGAACTTCCAGCCGGCTTC
TyrGluIleMetLeuGlyPheTyrGlyPheHisLeuGluAspArgGlyThrGlyAlaValCysArgAlaGlnAsnPheGlnProArgPhe 190

571 - CACAATCTGAACAGCCACAGCACAAACCTGGTATTACAGGCATCCTCAAGTCAGTGGTGAAGCTGGCTTAGAACACTACCAAGGCA
HisAsnLeuAsnSerHisSerHisAsnAsnLeuArgIleThrArgIleLeuLysSerLeuGlyGluLeuGlyLeuGluHistYrglnAla 220

661 - CCCCTGGCTCCGCTTCTTGAGGAGACCCCTGTAAGCACAAACTGCCCAAGCTGGCCAGACTGGCTGGACTACTTCCCTGTTGCT
ProLeuValArgPhePheLeuGluGluIleLeuValGlnHisLysLeuProSerValArgGlnSerAlaLeuAspTyrPheLeuPheAla 250

751 - GTGGCTGCCGACCCAGCCACTTGCCTGGGAGCTTGACTCTTGCCTGGCAGACTTCAAGCCCTGCCAGAGTTTGCTCTGGGGCCCGTGCAC
ValArgCysArgHisGlnArgArgGluLeuValTyrPheAlaTrpGluHisPheLeuThrGlyProArgGluProArgAsp 280

841 - AAGCTGGGAGATTCAAGCCCCAGACCATACCCAGCCACTTGCCTGGGAGCTTGACTCTGCCAGACACTGGAACAGCTGACGATGACGGATCCAGGGAC
LysLeuArgArgPheLysProGlnThrIleProLeuThrGlyProGlnProAspSerLeuAspProSerLeuAsn 310

931 - AAGAGGGCTGGCACCCAGGGTGGGACCTGTTGAAGGGACCTGTTGAGTGGGACGCTGAGTGGGACGACTGGGACGATGAGCTGGGAC
GlnGluAlaGlyThrGlnGlyArgAspLeuSerGlySerGlyArgAspLeuSerGlySerGlyAspSerGlyThrAlaGluAspProSerLeuAsn 340

1021 - ACAAAAGCCCTCAGATGGGGAAACCTGGATGGGAAACCTGGCTAACGAGCTAAGTCCCTGAGTCCCAGGGAGCAAGAAAGGAAGTGTG
ThrLysProSerAspGlyGlyThrLeuAspGlyAsnGlnArgAspGluAlaLysSerLeuSerProLysGluSerLysLysArgLysLeu 370

A

Figure 2A

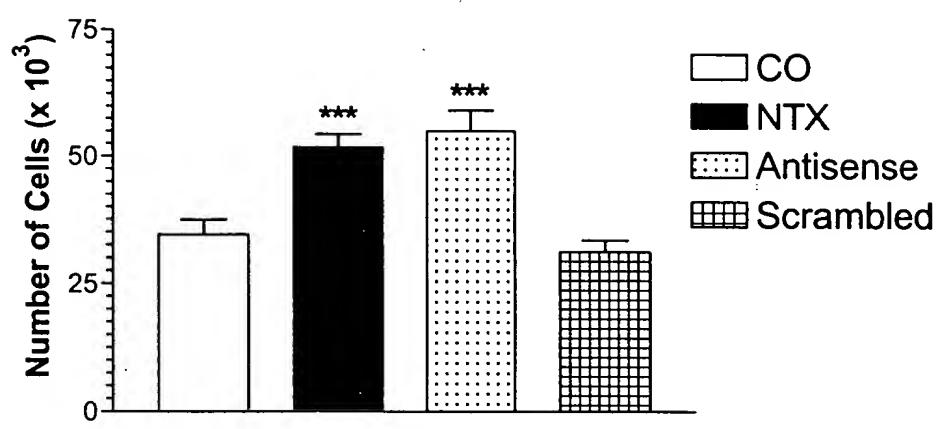


Figure 10

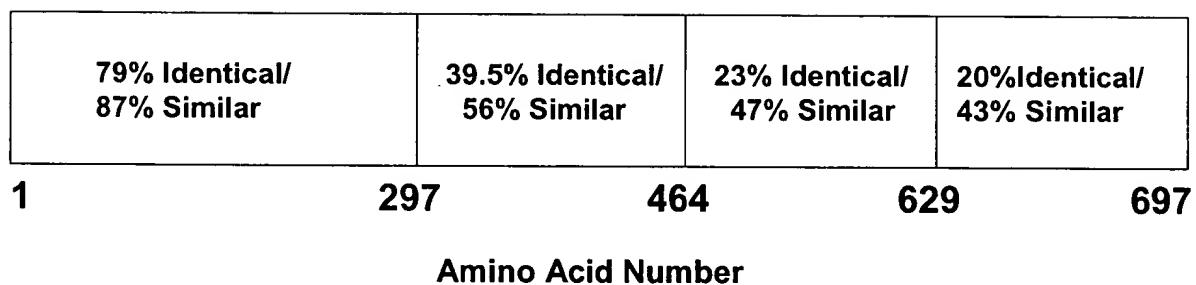


Figure 11

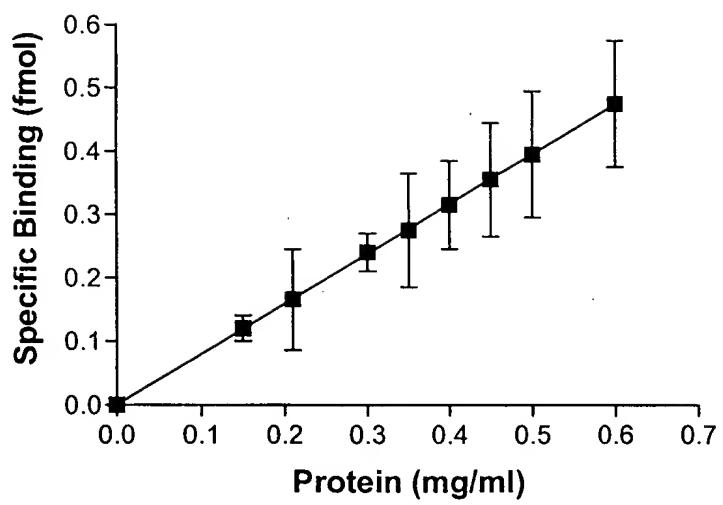


Figure 12

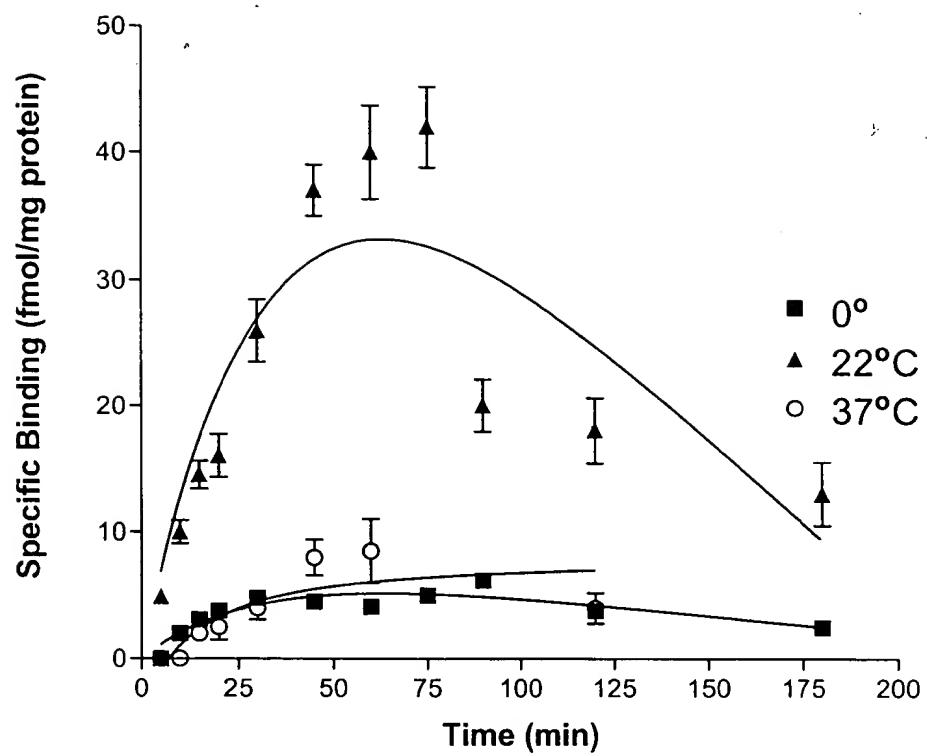


Figure 13

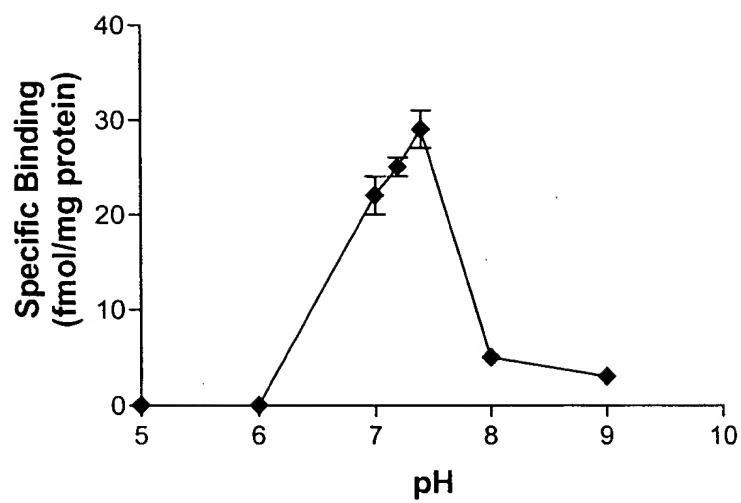


Figure 14

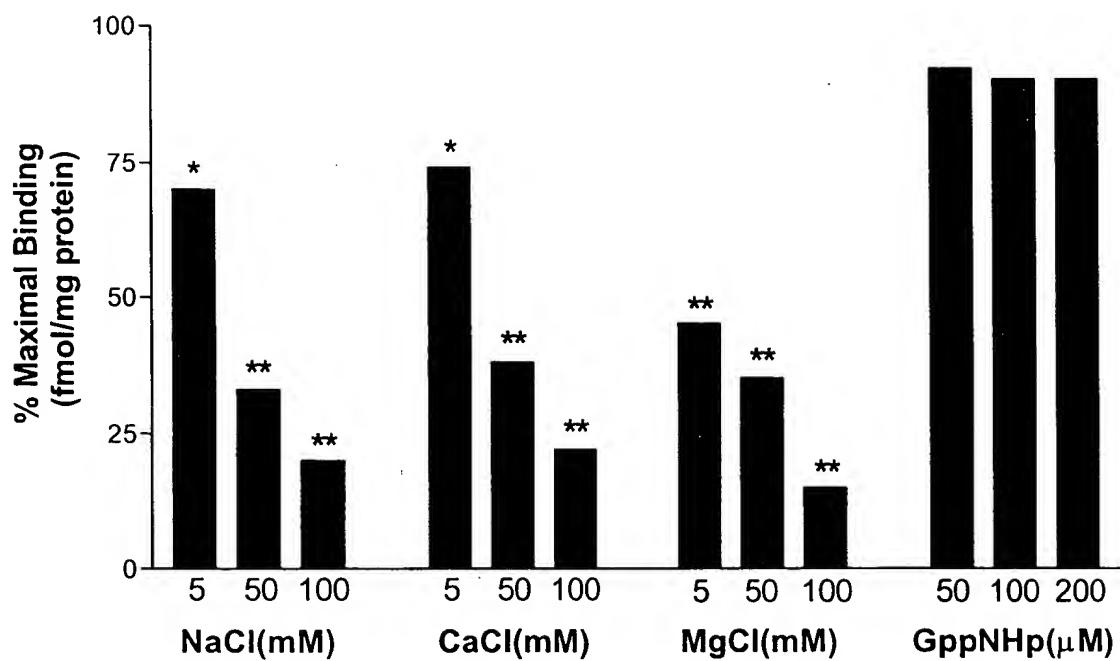


Figure 15

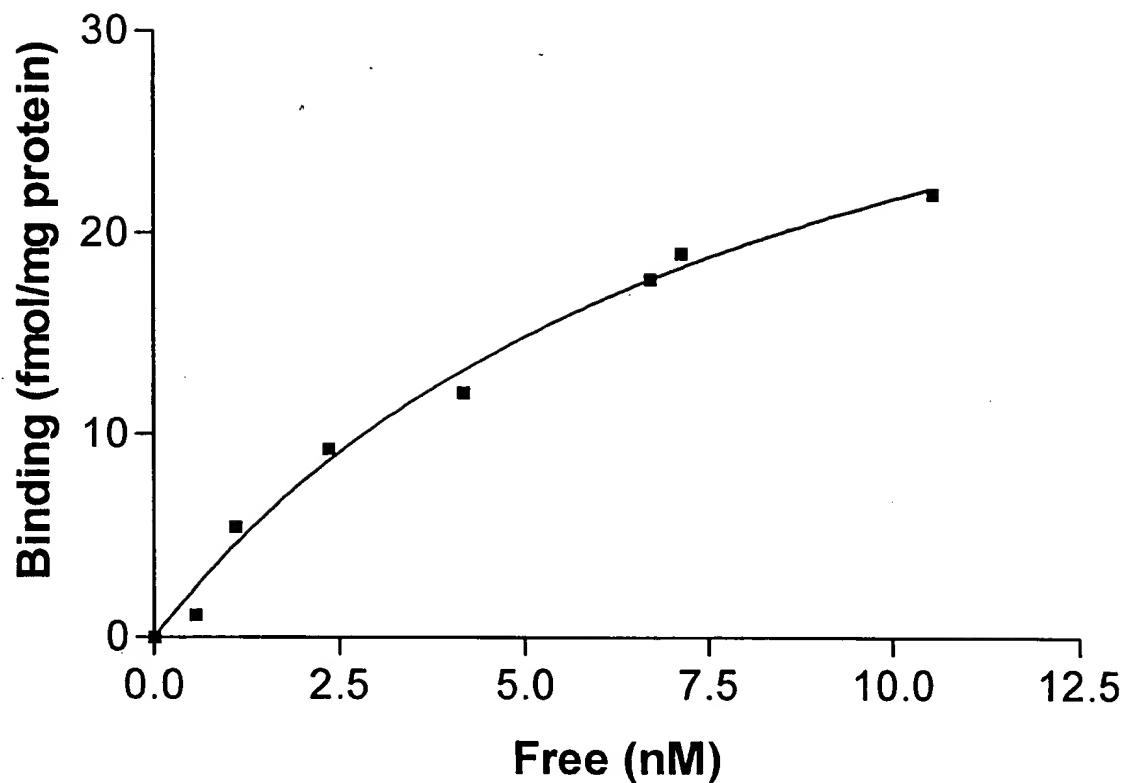


Figure 16A

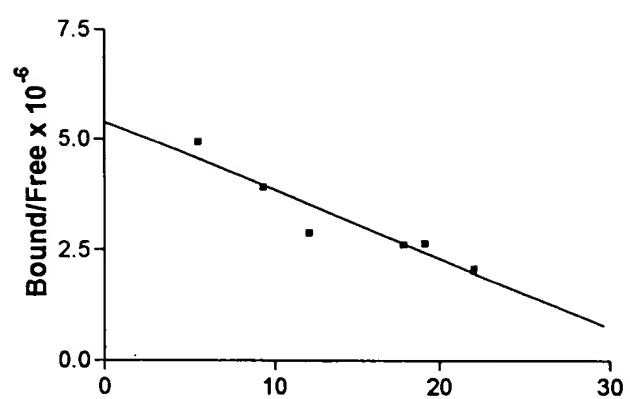
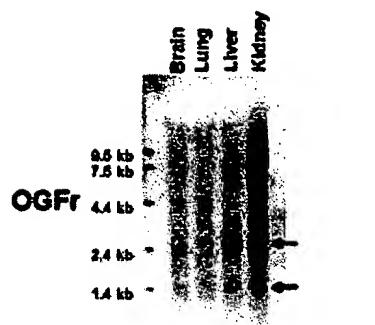


Figure 16B

Figure 9A



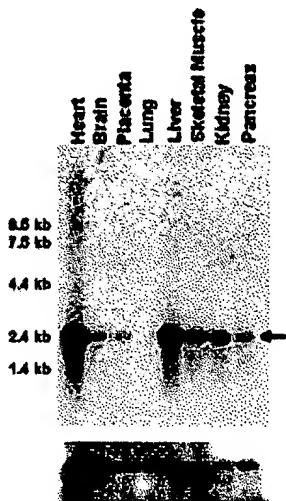
β -actin

Promyelocytic Leukemia HL-60
HeLa cell S3
Chronic Myelogenous Leukemia
Lymphoblastic Leukemia MOLT-4
Burkitt's Lymphoma Raji
Colonctal Adenocarcinoma SW480
Lung Carcinoma A549
Melanoma G361

OGFr

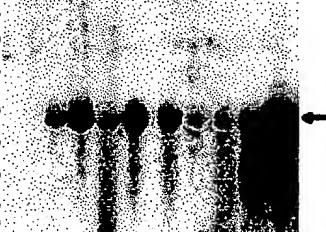
β -actin

Figure 9B



β -actin

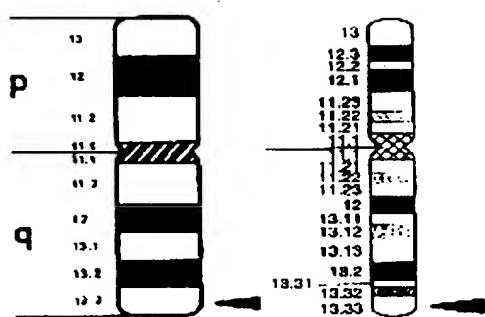
RNA Marker
BAPC-3
MIA-PaCa
CaR7
SK-N-SH
Human Tongue Cancer
Human Pancreas
Human Kidney
Human Renal Tumor
PANC-1



β -actin

Figure 9C

Figure 9D



20

Figure 8F

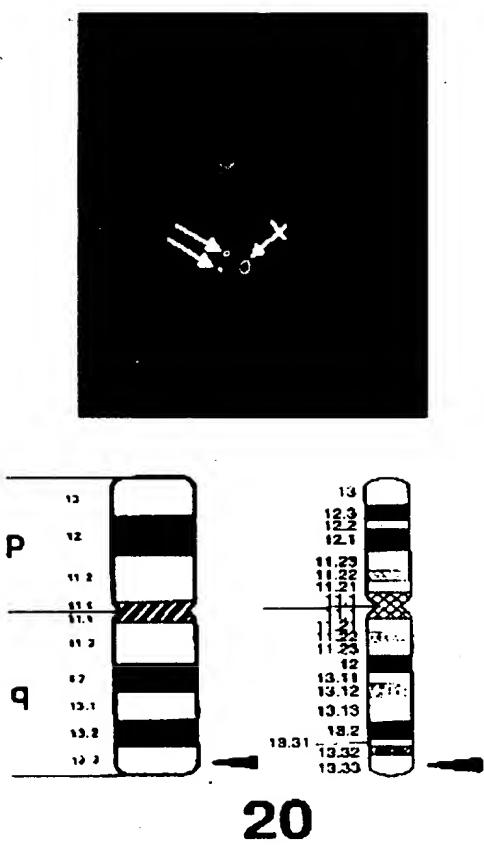
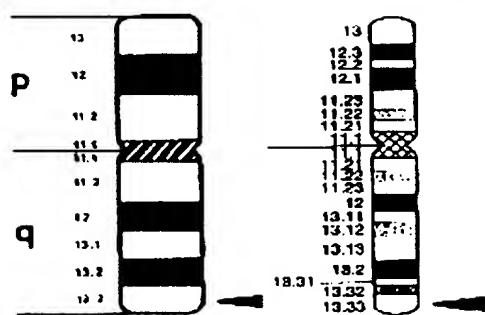


Figure 8F



20

Figure 8F

1	SPSPTGPSPAGPDEAESPSETPGPRA	↑	2
4	SPSPTGPSPAGPDEAESPSETPGPRA	↑	3
7	SPSPTGPSPAGPDEAESPSETPGPRA	↑	4
8	SPSPTGPSPAGPDEAESPSETPGPRA	↑	5

Figure 8E

7 SPSETPGSPAGPAGDEPAESPSETPGPRPA
4 SPSETPGSPAGPAGDEPAESPSETPGPRPA
8 SPSETPGSPAGPAGDEPAESPSETPGPRPA
GPAGDDEAESPSETPGRLPAGPAGDDEAETSESETGPSPAGPTRDEAE...
GPAGDDEAESPSETPGRLPAGPAGDDEAETSESETGPSPAGPTRDEAE...
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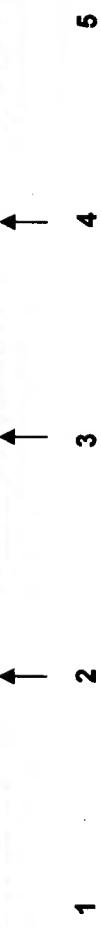


Figure 8E

Figure 8E



Figure 8D

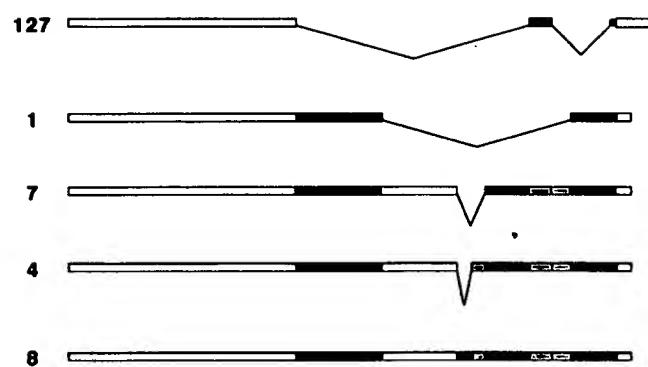


Figure 8C

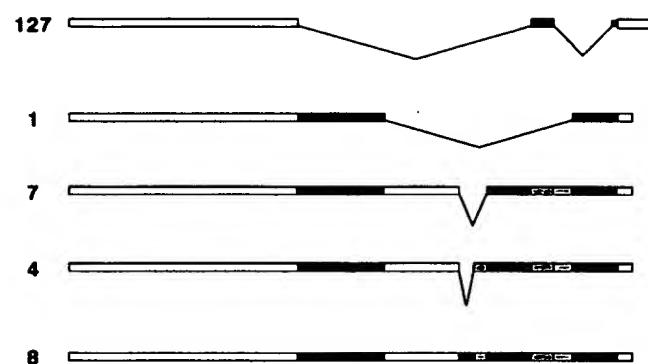


Figure 8C

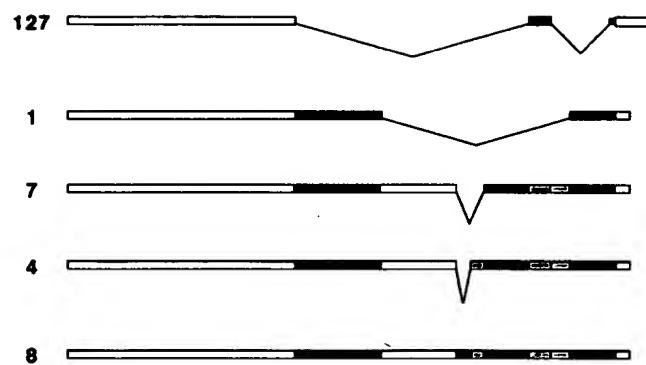


Figure 8C